

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 24, 2002, 11:24:03 ; Search time 05.25 seconds

Sequence: 1 MANOSICARLEPGALATKIO.....LMDLEQASQSSIKRPD 725
294,776 Million cell updates/sec

Scoring table: Gapop 10.0, Capet 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt.40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3683	99.9	725	MCAR_HUMAN	093661 homo sapien
2	3282	88.2	718	MCAR_CHICK	053909 ratialis
3	2856	77.5	671	KRP2_RAT	091636 homo sapien
4	2361	64.1	730	KCML_XENLA	000139 homo sapien
5	1888.5	50.7	619	KF2_HUMAN	028740 mus musculi
6	1839	50.4	716	KIF2_MOUSE	091637 xenopus lae
7	1839	50.4	716	KIF2_XENLA	024433 cyllindrophi
8	1750	46.2	632	KIF2_MOUSE	024433 cyllindrophi
9	574.5	15.6	1232	KF4_HUMAN	031712 mus musculi
10	574.5	15.6	1231	KF4_MOUSE	031712 mus musculi
11	569	15.4	1235	KF4_CHICK	090640 gallus galli
12	561.5	15.2	1056	K125_AYATH	082656 atrobipolis
13	527.5	15.0	1006	K125_TORAC	021854 xenopus lae
14	527.5	15.0	1006	K125_XENLA	091784 xenopus lae
15	519	14.1	1067	KF3A_HUMAN	051436 xenopus lae
16	515	14.0	1072	KF3A_HUMAN	091783 xenopus lae
17	512.5	13.9	1067	KF3A_XENLA	091783 xenopus lae
18	509.5	13.8	1067	KF3A_MOUSE	091783 xenopus lae
19	506	13.7	1067	BES1_XENLA	028742 xenopus lae
20	502	13.6	1117	BES1_HUMAN	028742 xenopus lae
21	502	13.6	1117	BES1_MOUSE	028742 xenopus lae
22	498	13.5	1055	KF6_MOUSE	028742 xenopus lae
23	493.5	13.4	956	KF5C_MOUSE	028742 xenopus lae
24	491	13.3	957	KF5C_HUMAN	028742 xenopus lae
25	491	13.3	1690	KF1A_HUMAN	012756 homo sapien
26	489.5	13.3	1106	KF1A_MOUSE	012756 homo sapien
27	489.5	13.3	1106	KF1A_XENLA	012756 homo sapien
28	488	13.2	1699	K122_STRPD	048836 mus musculi
29	488	13.2	1695	KF1A_MOUSE	048836 mus musculi
30	478.5	13.0	955	K1N1_MOUSE	048836 mus musculi
31	478	13.0	786	F110_CHARE	048836 mus musculi
32	477	12.9	1816	KF1B_MOUSE	060575 mus musculi
33	473	12.8	747	KF1B_MOUSE	060575 mus musculi

Result No.	Score	Query Match	Length	DB ID	Description
34	472	12.8	747	KF3B_HUMAN	015066 homo sapien
35	468	12.7	142	K121_STRPD	015066 homo sapien
36	467.5	12.6	1364	K121_MOUSE	015066 homo sapien
37	467.5	12.6	1364	K121_XENLA	015066 homo sapien
38	466	12.6	967	KF1B_MOUSE	035787 ratius norv
39	463.5	12.6	784	K128_MOUSE	015066 homo sapien
40	463	12.6	796	KF3C_RAT	055165 ratialis
41	462.5	12.6	1184	K1N1_MOUSE	035066 mus musculi
42	458	12.4	796	KF1C_MOUSE	035066 mus musculi
43	458	12.4	1816	KF1B_MOUSE	060575 mus musculi
44	457.5	12.4	1816	KF1B_MOUSE	060575 mus musculi
45	457	12.4	975	K1N1_MOUSE	035066 mus musculi

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	3683	99.9	725	MCAR_HUMAN	093661 homo sapien
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13	527.5	15.0	1006	K125_TORAC	021854 xenopus lae
14	527.5	15.0	1006	K125_XENLA	091784 xenopus lae
15	519	14.1	1067	KF3A_HUMAN	051436 xenopus lae
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17	512.5	13.9	1067	KF3A_XENLA	091783 xenopus lae
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20	502	13.6	1117	BES1_HUMAN	028742 xenopus lae
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26	489.5	13.3	1106	KF1A_MOUSE	012756 homo sapien
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29	488	13.2	1695	KF1A_MOUSE	048836 mus musculi
30	478.5	13.0	955	K1N1_MOUSE	048836 mus musculi
31	478	13.0	786	F110_CHARE	048836 mus musculi
32	477	12.9	1816	KF1B_MOUSE	060575 mus musculi
33	473	12.8	747	KF1B_MOUSE	060575 mus musculi

QY 121 PITGVSAAVERNPAYVNTSOPICAKPIYTDIEDIKROEPOVYRKKEEALMADILSR 180
 DB 124 PITGVSAAVERNPAYVNTSOPICAKPIYTDIEDIKROEPOVYRKKEEALMADILSR 183
 QY 181 AADTEEDIDIDSGDEA 197
 DB 184 AADTEEDIDIDSGDEA 200

RESULT 2

Q90B5 PRELIMINARY: PRT: 411 AA.

DC 01-MAY-2000 (TRENDArel. 13, Created)
 DT 01-MAY-2000 (TRENDArel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENDArel. 17, Last annotation update)
 DE METHYL-CPG BINDING PROTEIN 2.
 GN MBD2.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=98449942; PubMed=10441743;
 RT Hendrich B., Bird A.;
 *Identification and characterization of a family of mammalian methyl-
 CPG binding proteins.
 RL Mol. Cell. Biol. 18:6538-6547(1998).
 DB EMBL: AF120988; AAD56597.1; JOINED.
 DB EMBL: AF120989; AAD56597.1; JOINED.
 DB EMBL: AF120990; AAD56597.1; JOINED.
 DB EMBL: AF120991; AAD56597.1; JOINED.
 DB EMBL: AF120992; AAD56597.1; JOINED.
 DB EMBL: AF120993; AAD56597.1; JOINED.
 DR Interpro: IPRO01739; MBD: 1.
 DR Pfam: PF01429; MBD: 1.
 DR SMART: SM00391; MBD: 1.
 SQ SEQUENCE 411 AA: 43254 MW: 463550CF9BA0F5FA CRC64;

Query Match 100.0%; Score 998; DB 4; Length 411;

Best Local Similarity 100.0%; Pred. No. 2,676; Mismatches 0; Indels 0; Gaps 0;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PSKLNKORLNDPILNKGKEDLTLPIROTISIFKOPVYKVTNHSNKYSQDROM 60
 DB 213 PSKLNKORLNDPILNKGKEDLTLPIROTISIFKOPVYKVTNHSNKYSQDROM 274
 QY 61 NEQPOLFWERKLOGLSASDVEDIITKIMELPKGLGVGSNDETLLSVAVALHTSSA 120
 DB 275 NEQPOLFWERKLOGLSASDVEDIITKIMELPKGLGVGSNDETLLSVAVALHTSSA 334
 QY 121 PITGVSAAVERNPAYVNTSOPICAKPIYTDIEDIKROEPOVYRKKEEALMADILSR 180
 DB 335 PITGVSAAVERNPAYVNTSOPICAKPIYTDIEDIKROEPOVYRKKEEALMADILSR 394
 QY 181 AADTEEDIDIDSGDEA 197
 DB 395 AADTEEDIDIDSGDEA 411

RESULT 3 PRELIMINARY: PRT: 414 AA.

Q92ZEL

AC Q92ZEL; (TRENDArel. 10, Created)
 DT 01-MAY-1999 (TRENDArel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENDArel. 17, Last annotation update)
 DE METHYL-CPG BINDING PROTEIN MBD2.
 GN MBD2.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=98449942; PubMed=9774669;
 RT Hendrich B., Abbott C., McQueen H., Chambers D., Cross S., Bird A.;
 *Identification and characterization of a family of mammalian methyl-
 CPG binding proteins.
 RL Mol. Cell. Biol. 18:6538-6547(1998).
 DB EMBL: AF120985; AAD50372.1; JOINED.
 DB EMBL: AF120986; AAD50372.1; JOINED.
 DB EMBL: AF120987; AAD50372.1; JOINED.
 DB EMBL: AF120988; AAD50372.1; JOINED.
 DB EMBL: AF120989; AAD50372.1; JOINED.
 DB EMBL: AF120990; AAD50372.1; JOINED.
 DB EMBL: AF120991; AAD50372.1; JOINED.
 DB EMBL: AF120992; AAD50372.1; JOINED.
 DB EMBL: AF120993; AAD50372.1; JOINED.
 DR Interpro: IPRO01739; MBD: 1.
 DR Pfam: PF01429; MBD: 1.
 DR SMART: SM00391; MBD: 1.
 SQ SEQUENCE 414 AA: 43543 MW: 960195E3A7B8E53 CRC64;

Query Match 98.8%; Score 986; DB 11; Length 414;

Best Local Similarity 98.5%; Pred. No. 2,767; Mismatches 1; Indels 0; Gaps 0;

Matches 194; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSKLNKORLNDPILNKGKEDLTLPIROTISIFKOPVYKVTNHSNKYSQDROM 60
 DB 218 PSKLNKORLNDPILNKGKEDLTLPIROTISIFKOPVYKVTNHSNKYSQDROM 277
 QY 61 NEQPOLFWERKLOGLSASDVEDIITKIMELPKGLGVGSNDETLLSVAVALHTSSA 120
 DB 278 NEQPOLFWERKLOGLSASDVEDIITKIMELPKGLGVGSNDETLLSVAVALHTSSA 337
 QY 121 PITGVSAAVERNPAYVNTSOPICAKPIYTDIEDIKROEPOVYRKKEEALMADILSR 180
 DB 338 PITGVSAAVERNPAYVNTSOPICAKPIYTDIEDIKROEPOVYRKKEEALMADILSR 397
 QY 181 AADTEEDIDIDSGDEA 197
 DB 398 AADTEEDIDIDSGDEA 414

RESULT 4

Q90B5 PRELIMINARY: PRT: 282 AA.

DC 01-MAY-2000 (TRENDArel. 13, Created)
 DT 01-MAY-2000 (TRENDArel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENDArel. 17, Last annotation update)
 DE METHYL-CPG BINDING PROTEIN MBD3.
 GN MBD3.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 NCBI_TaxID=8155;

DB 135 H10K0FHNERSRVRVDAALDLFTTGCIARHOLAPRNLCSPEPVSPVKICFDL 194
 OY 63 GSGMKLNNSCTPTITTELTTPGCSAEYAAPEVEFTPOATPYDKRDLMSGLGVYIL 120
 DB 193 GSGMKLNNSCTPTITTELTTPGCSAEYAAPEVEFTPOATPYDKRDLMSGLGVYIL 234
 OY 121 SCTPPYRGAGDCCMGDNGEYVQCNKLPESIOGKTEFPKDMANISPAADISKLL 180
 DB 255 SCTPPYRGAGDCCMGDNGEYVQCNKLPESIOGKTEFPKDMANISPAADISKLL 314
 OY 181 VDAKOKLSAAOVLOHPVWGGAPEPGIPPOVLONSSTMDLTFAPAAIALNOLSOH 240
 DB 315 VDAKOKLSAAOVLOHPVWGGAPEPGIPPOVLONSSTMDLTFAPAAIALNOLSOH 374
 OY 241 EENELAEERPALADGICSMKLSPPCKSLARRRALLAQNGENSPPTL 290
 DB 375 EENELAEERPALADGICSMKLSPPCKSLARRRALLAQNGENSPPTL 424

RESULT 2
 OY09B05 PRELIMINARY: PRT: 465 AA.
 AC O9B05;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SUMMARY: HOMOGENEOUS INTERACTING SERINE/THREONINE KINASE 1.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
 NX NCBI_TaxID=9606;
 RA SOURCE FROM N.A.
 RC STISSID=PLACENTA, CHROMOCENTROMA.
 RA Streuberg R.;
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: BC002155; AM00755.1; -
 DR Genbank: U0002290; Euk.plkase.
 DR Interpro: IPR002290; Ser.thr.pkinase.
 DR Refseq: P00069; Plkasee; 1.
 DR Pfam: PF00069; Plkasee; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN.1.
 DR PROSITE: PS00108; PROTEIN KINASE; DOM.1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 465 AA: 51343 MW: 542250.35 CD343 CR64.

Query Match 97.5%: Score 1497.5; DB 4; Length 465;
 Best Local Similarity 97.5%: Pctid. No. 8-2e-133;
 Matches 288: Conservative 2; Mismatches 0; Indels 41; Gaps 1;

DB 375 OQAPKPKALPTPOVLONSSTMDLTFAPAAIALNOLSOHEENELAEERPALADGICSM 434
 OY 260 KISPPCKSLARRRALLAQNGENSPPTL 290
 DB 435 KISPPCKSLARRRALLAQNGENSPPTL 465

RESULT 3
 OY09B05 PRELIMINARY: PRT: 415 AA.
 AC O9B05;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SUMMARY: HOMOGENEOUS INTERACTING KINASE.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RA SOURCE FROM N.A.
 RC STISSID=SPLEEN, PubMed-9155017;
 RA Maskiewicz 1990B; Flynn 1990; Cooper J.A.;
 RT Kinase Mnk1 and Mnk2.
 RL EMBL J. 15:1905-1920(1997).
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: U03450; U03451; U03452; U03453; U03454; U03455; U03456; U03457; U03458; U03459; U03460; U03461; U03462; U03463; U03464; U03465; U03466; U03467; U03468; U03469; U03470; U03471; U03472; U03473; U03474; U03475; U03476; U03477; U03478; U03479; U03480; U03481; U03482; U03483; U03484; U03485; U03486; U03487; U03488; U03489; U03490; U03491; U03492; U03493; U03494; U03495; U03496; U03497; U03498; U03499; U03500; U03501; U03502; U03503; U03504; U03505; U03506; U03507; U03508; U03509; U03510; U03511; U03512; U03513; U03514; U03515; U03516; U03517; U03518; U03519; U03520; U03521; U03522; U03523; U03524; U03525; U03526; U03527; U03528; U03529; U03530; U03531; U03532; U03533; U03534; U03535; U03536; U03537; U03538; U03539; U03540; U03541; U03542; U03543; U03544; U03545; U03546; U03547; U03548; U03549; U03550; U03551; U03552; U03553; U03554; U03555; U03556; U03557; U03558; U03559; U03560; U03561; U03562; U03563; U03564; U03565; U03566; U03567; U03568; U03569; U03570; U03571; U03572; U03573; 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OK protein - protein search, using sw model

Run on: July 24, 2002, 11:10:27 ; Search time 346.34 seconds

28,073 Million cell updates/sec

Title: PCT-US02-13994-18

Perfect score: 4677

Sequence: 1 EFLSKSKREPTFGSLNLSIP.....ACLGNSLGNAGTEPEAK 997

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 74754 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 74754

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

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22: /SIDSL/gcdata/hold-geneseq/geneeq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4669	99.8	887	20	AAV7092
2	4651	99.4	1141	21	AAH4006
3	3512	75.1	716	22	AAH4958
4	2662	56.5	967	22	AAH4957
5	2012	43.2	917	22	AAH4956
6	1818	38.9	1008	22	AAH4955
7	1818	38.9	1008	22	AAH4954
8	1732	37.0	1428	21	AAV7093
9	1594	34.1	614	22	AAH4953
10	1591.5	33.3	1235	22	AAH4952
11	1559.5	33.3	574	21	AAV7092

12	1515	32.4	541	21	AAH4945
13	1247	26.7	328	21	AAH4571
14	1090	23.3	327	21	AAH4574
15	945	20.2	191	22	AAH4542
16	898	19.2	276	22	AAH4538
17	724.5	15.7	76	22	AAH4535
18	724.5	15.7	76	22	AAH4534
19	701.5	15.0	552	21	AAH4531
20	697.5	14.9	499	21	AAH4529
21	695.5	14.9	468	21	AAH4527
22	693.5	14.8	552	21	AAH4526
23	689.5	14.7	499	21	AAH4525
24	680.5	14.7	468	21	AAH4524
25	660.5	14.7	468	21	AAH4523
26	641.5	13.7	817	22	AAH4522
27	631	13.3	675	21	AAH4521
28	621	13.3	686	21	AAH4520
29	573.5	12.3	330	22	AAH4519
30	547	11.3	363	22	AAH4518
31	527	10.3	363	22	AAH4517
32	451	9.6	174	22	AAH4516
33	451	9.6	174	22	AAH4515
34	445	9.5	164	21	AAH4514
35	374.5	8.0	335	20	AAH4513
36	371.5	7.9	398	21	AAH4512
37	363	7.8	364	21	AAH4511
38	352	7.5	337	21	AAH4510
39	303.5	6.5	433	22	AAH4509
40	303.5	6.5	433	22	AAH4508
41	302	6.5	482	17	AAH4507
42	300	6.4	482	18	AAH4506
43	300	6.4	482	22	AAH4505
44	300	6.4	482	22	AAH4504
45	300	6.4	488	21	AAH4503

ALIGNMENTS

RESULT 1	AAV7092	standard: Protein: 997 AA.
ID	AAV7092	
AC	AAV7092	
XX	02-JUL-1999 (first entry)	
XX	Colon cancer associated antigen precursor sequence.	
XX	Cancer associated antigen: diagnosis; research; treatment; human.	
XX	breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer.	
XX	Homologous.	
XX	WO9004265-A2.	
XX	15-JUL-1998	98MO-0314679.
XX	22-JUN-1998	98US-0102322.
XX	17-OCT-1997	97US-0896164.
XX	10-OCT-1997	97US-0061599.
XX	10-OCT-1997	97US-0061765.
XX	11-OCT-1997	97US-0048705.
XX	11-OCT-1997	97US-0021697.
XX	(LUDWIG) LUDWIG INSTR CANCER RES.	
XX	Chen Y., Gout I., Gure A., O'Hare M., Ohta Y., Old L., Pitman-Smith M., Sahin U., Scanlan M., Stockert E., Tureci O.	

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OM protein - protein search, using sw model

Run on: July 24, 2002, 11:10:51 : Search time 346.34 Seconds

(Without alignments)
241,173 Million cell updates/sec

Title: BCT-US02-13994-21

Sequence: 3941
1 RVKATLSERIDSCDKLP.....EASTWYGIIFPNRIPTL 752

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying Chosen Parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 100
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMILARITIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394.1	100.0	752	AAV07108	Human cancer assoc
2	318.5	95.7	752	AAV07108	Human cancer assoc
3	273.5	92.5	752	AAV07108	Human cancer assoc
4	273.5	6.9	777	AAU07898	Polypeptide sequen
5	268	6.8	928	AAU07898	Polypeptide sequen
6	191.5	4.9	1098	AAU03596	Human ORX ORF1722
7	176	4.5	579	AAU03596	Human ORX ORF1722
8	166	4.2	3245	AAU03596	Kinecrosin protein
9	166	4.2	3245	AAU03596	Human microin amin
10	165	4.2	2482	AAU03596	Human microin amin
11	160.5	4.1	633	AAU03596	Human protein sequ

12	146.5	3.7	926	22	ABR62874
13	141	3.6	1019	22	AAU07892
14	139.5	3.5	1160	22	ABG17343
15	138.5	3.5	1180	22	ABG17343
16	138	3.5	944	22	ABG06345
17	136	3.5	1513	14	ABR43353
18	135	3.4	355	21	AAU07715
19	135	3.4	429	21	AAU07715
20	135	3.4	496	21	AAU07715
21	135	3.4	1788	22	AAU03596
22	133	3.4	931	21	AAU03596
23	133	3.4	937	21	AAU03596
24	133	3.4	985	21	AAU03596
25	133	3.4	2025	22	AAU04207
26	133	3.4	2098	21	AAU15924
27	133	3.4	1328	15	AAU08875
28	132.5	3.4	1786	18	AAU04790
29	132.5	3.4	1786	18	AAU04790
30	132.5	3.4	1786	18	AAU04790
31	132	3.3	976	21	AAU03596
32	132	3.3	1979	21	AAU18171
33	131.5	3.3	1433	18	AAU14517
34	131.5	3.3	2048	22	AAU00527
35	131.5	3.3	1328	15	AAU08875
36	131.0	3.3	129.5	3.3	AAU09026
37	129.5	3.3	864	22	AAU09026
38	129	3.3	391	22	AAU03056
39	129	3.3	1049	22	ABR5817
40	128	3.2	1096	22	ABR5817
41	127.5	3.2	2271	22	ABR5817
42	127.5	3.2	2271	22	ABR5817
43	127	3.2	745	22	ABR6722
44	126.5	3.2	1124	21	AAU05179
45	126.5	3.2	1703	21	AAU05179

ALIGNMENTS

RESULT	1	ALIGNMENTS
AAV07108	AAV07108 standard: Protein: 752 AA.	
ID	AAV07108	
XX	AAV07108:	
XX	02-JUL-1999 (first entry)	
DE	Colon cancer associated antigen precursor sequence.	
XX	Cancer associated antigen: diagnosis; research; treatment: human;	
XX	prostate cancer; colon cancer; gastric cancer; renal cancer; lung cancer;	
XX	prostate cancer.	
XX	Homologous.	
OS	Homologous.	
XX	28-JAN-1999.	
XX	15-JUL-1998: 98MO-0514679.	
XX	22-JUN-1998: 98MO-0102322.	
XX	17-JUL-1997: 97MO-0886164.	
XX	10-OCT-1997: 97MO-0611765.	
XX	10-OCT-1997: 97MO-0611765.	
XX	11-OCT-1997: 97GB-0021697.	
XX	(LUDWIG) LUDWIG INST CANCER RES.	
XX	Chen Y, Gove J, Gove A, O'Hare M, Ohta Y, Old LJ,	
XX	Pfeundach M, Sahlin U, Scanlan MJ, Stockert E,	
XX	Tureci O,	

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Polypeptide sequen
Novel human diapo
Novel human diapo
Novel human diapo
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P. falciparum liver
Human SCP-1, nuclein
Plasmodium falcipa
Human WRN gene pro
Human polypeptide
Drosophila melanog
Drosophila melanog
Human polypeptide
Novel human diapo
Drosophila melanog
Drosophila melanog
Human polypeptide
S. cerevisiae DNA
Cellulose synthase
Arabidopsis thalia

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM protein - protein search, using SW model

Run on: July 24, 2002, 11:11:01 : Search time 346.34 Seconds
(without alignments)
63.179 Million cell updates/sec

Title: PCT-US02-13994-23
Perfect score: 1 PSL0KNKGRRLRDLNOKR.....LSBAADREMDIEMSDGA 197
Sequence: 998

Scoring table: BLOSUM62
Gapop 10.0, Capopt 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	998	100.0	200	AAV07107	Colton cancer assoc
2	998	100.0	281	AAV18329	Human secreted pro
3	998	100.0	281	AAV18329	Human secreted pro
4	998	100.0	281	AAV18329	Human prostate can
5	998	100.0	411	AAV14197	Human DNA demethyl
6	998	100.0	411	AAV14197	Human protein sequ
7	998	100.0	411	AAV43314	Human protein 81
8	998	100.0	411	AAV43314	Heart muscle cell
9	998	100.0	411	AAV43314	Heart muscle cell
10	998	100.0	411	AAV43314	Heart muscle cell
11	746	74.9	291	AAV14196	Human DNA demethyl

13	739.5	74.1	285	20	AAV14200
14	739	74.0	218	22	AAV37373
15	340.5	34.1	226	22	AAV37373
16	340.5	34.1	226	22	AAV37373
17	340.5	34.1	226	22	AAV37373
18	107.5	10.8	1028	22	AAV17916
19	95.5	9.6	914	18	AAV53802
20	95.5	9.6	914	18	AAV53802
21	95.5	9.6	914	18	AAV53802
22	95.5	9.6	914	18	AAV53802
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24	89.91	9.1	1049	21	AAV68823
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27	88.5	8.9	1203	22	AAV72824
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29	88.5	8.9	1203	22	AAV72824
30	88.5	8.9	1203	22	AAV72824
31	87.5	8.8	1406	22	AAV37278
32	87.5	8.8	1406	22	AAV37278
33	87.5	8.8	1406	22	AAV37278
34	87.5	8.8	1406	22	AAV37278
35	87.5	8.8	1406	22	AAV37278
36	86.5	8.7	5096	22	AAV63153
37	86.5	8.7	5096	22	AAV63153
38	86.5	8.7	5096	22	AAV63153
39	86.5	8.7	5096	22	AAV63153
40	86.5	8.7	5096	22	AAV63153
41	86.5	8.7	5096	22	AAV63153
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44	86.5	8.7	5096	22	AAV63153
45	86.5	8.7	5096	22	AAV63153

ALIGNMENTS

RESULT 1
AAV07107 standard: Protein: 200 AA.
AAV07107:
02-JUL-1998 (first entry)
Colton cancer associated antigen precursor sequence.
Cancer associated antigen: diagnosis; research; treatment: human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
prostate cancer.
Homo sapiens.
MO9904265-A2.
28-JAN-1999.
15-JUL-1998: 98MO-US14679.
22-JUN-1998: 98US-0102322.
17-JUL-1997: 97US-0896164.
10-OCT-1997: 97US-0061599.
10-OCT-1997: 97US-0048705.
11-OCT-1997: 97GB-0021697.
(LUDM-) LUDMIG INST CANCER RES.
Chen Y, Gout I, Gure A, O'Hare M, Obara Y, Old LJ,
Pridemore M, Saito U, Scanlan NU, Stockert E,
Turel O.

Mouse DNA demethyl
Human protein sequ
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Human SC2 protein
Human staxin-2, H
Human acid sequenc
Human ORF2808
Human protein SPO
Drosophila melanog
Spinocerebellar at
A. thaliana enviro
Human protein sequ
Human protein sequ
Drosophila melanog
Drosophila melanog
Mouse protein sequ
Human ORF1689
Human ORF1689
Drosophila melanog
Arabidopsis thalian
Arabidopsis thalian
Arabidopsis thalian
Human peptide 1965
Peptide 1965 encod
Human protein 1965
Human bone marrow

XX
DR 1999-132446/11.

XX
PT New isolated cancer associated nucleic acids and polypeptides -
PT Isolated using sera from cancer patients, used to develop products
PT for the diagnosis, monitoring or treatment of cancers

XX
PT Disclosure: Page 677: 787pp. English.

XX
CC The invention relates to a method for diagnosing a disorder characterized
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product of the NAM, and (b) detecting the binding of the agent to the
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterized by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC cancer associated antigen precursors expressed in human breast
CC cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer.

XX
CC Sequence 200 AA:

Query Match 100.0% Score 988 DB 20 Length 200
Best Local Similarity 100.0% Prod No 7 4e-91

Matches 197: Conservative 0 Mismatches 0 Indels 0 Gaps 0:

OY 1 PSLQKNNKRLNDELNKKNGKPKDNLTLPTKSTISIFKQPTVKNPSPNVASPOPM 60
DB 4 PSLQKNNKRLNDELNKKNGKPKDNLTLPTKSTISIFKQPTVKNPSPNVASPOPM 63
OY 61 NEQPOLFWERLQGLASDSTQITKTEWELKGLQGPSNDRTLLSASALITSSA 120
DB 64 NEQPIQLFEKRLQGLASDSTQITKTEWELKGLQGPSNDRTLLSASALITSSA 123
OY 121 PRTQGSAAVKNPAVWMTSOPILKAFVTDENIRKQSERVQGVKRTLEALMADLSR 180
DB 124 PRTQGSAAVKNPAVWMTSOPILKAFVTDENIRKQSERVQGVKRTLEALMADLSR 183
OY 181 ADTEEDIDEDSGDE 197
DB 184 ADTEEDIDEDSGDE 200

RESULT 2

AAW74980
ID AAW74980 standard: Protein: 263 AA.

XX
XX AAW74980:

DI 25-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 106 clone HT3AM5.

XX Human: secreted protein; testis; tumour; foetal brain tissue;

XX K562 cell line; cancer; central nervous system; seizure;

XX diagnosis; neurodegenerative disease.

OS Homo sapiens.

XX Key Location/Qualifiers

XX MISC-difference 253

XX /Index- unknown

XX MO9839448-AA.

XX 11-SEP-1998.

XX 06-MAR-1998.

XX 98NC-US04493.

XX 02-OCT-1997 97US-0061060
XX 07-MAR-1997 97US-0061061
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OK protein - protein search, using sw model

Run on: July 24, 2002, 11:10:35 : Search time 346.34 seconds

Database: 385,430 Million cell updates/sec

Title: PCT-US02-13994-19

Perfect score: 4413

Sequence: 1 MWDHCEELKLSSEVFQDM.....RQDQDKKQGTFAVLVNT 990

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 74/574 seqs, 11073796 reads

Total number of hits satisfying chosen parameters: 74/574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	4016	91.0	1068	21	AA199273			Human huntingtin-1
2	3296	74.7	676	21	AA199271			Human huntingtin-1
3	2014.5	45.6	1090	21	AA199270			Human huntingtin-1
4	2009.5	45.5	914	18	AA18030			Human huntingtin-1
5	2009.5	45.5	914	18	AA18030			Human huntingtin-1
6	13400	31.7	283	22	AA056132			Human protein segn
7	896.5	20.3	1087	22	AB053558			Drosophila melanog
8	896.5	20.3	1087	22	AB053559			Drosophila melanog
9	718.5	16.3	388	18	AA18029			Human huntingtin-1
10	705.5	16.0	388	21	AA19268			Human huntingtin-1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the one obtained. The results are sorted and are derived by analysis of the total score distribution.

Result	No.	Score	Query	Match	Length	DB	ID	Description
12	375.5	8.5	2541	21	AA041087			Human ORF1
13	358	8.1	1134	22	AA076810			Human protein S80
14	358	8.1	1144	22	AA039293			Human polyprotein
15	358	8.1	1165	22	AA039312			Human polyprotein
16	353	8.0	2836	22	AB062719			Drosophila melanog
17	348	7.9	1177	22	AA079794			Human protein S80
18	348	7.9	1177	22	AA041098			Human polyprotein
19	348	7.9	1177	22	AA041098			Human polyprotein
20	332	7.5	2101	21	AA149936			Human NMDA protein
21	336	7.4	2192	18	AA121732			Leu/tyrosine fuction p
22	336	7.4	2272	18	AA021331			GAL4/NMDA fuction p
23	335	7.4	1154	22	AA032042			Novel human secret
24	335	7.4	1154	22	AA032042			Novel human secret
25	335	7.4	1154	22	AA032042			Novel human secret
26	335	7.4	1154	22	AA032042			Novel human secret
27	332	7.3	1690	22	AB061144			Drosophila melanog
28	332	7.3	1690	22	AB061173			Drosophila melanog
29	332	7.3	2101	15	AA072773			Sequence of the 1n
30	332	7.3	2101	15	AA072773			Nucleic acid
31	332	7.3	2101	15	AA072773			Human NMDA protein
32	332	7.3	2101	15	AA072773			Human NMDA protein
33	332	7.3	2101	15	AA072773			Human NMDA protein
34	330	7.3	118	22	AA018821			Novel prostate gla
35	330	7.3	118	22	AA018821			Novel prostate gla
36	318	7.2	2246	22	AA050580			Novel human dispo
37	316.5	7.2	1663	22	AA079838			Human protein S80
38	312.5	7.1	2444	21	AA077565			Human cytoskeletal
39	312.5	7.1	2444	21	AA077565			Human cytoskeletal
40	311.5	7.1	1988	22	AA041000			Human polyprotein
41	305.5	6.9	1083	22	AB020032			Novel human dispo
42	305.5	6.9	1083	22	AB020032			Novel human dispo
43	302	6.8	1879	22	AA057550			Human protein segn
44	299.5	6.8	1489	22	AB059448			Drosophila melanog
45	298.5	6.8	2056	22	AB059448			Drosophila melanog

ALIGNMENTS

RESULT 1
AA199273 standard: Protein: 1068 AA.
XX
AC AA199273:
XX
DT 17-APR-2000 (first entry)
XX
AC Mouse huntingtin-interacting protein (mHtIP).
XX
KX Mouse huntingtin-interacting protein (mHtIP).
XX
KM Huntingtin interacting Protein: HtIP: death effector domain; DBD: human.
XX
KM Apoptosis: HtIP: apoptosis modulating protein; cell death; gene therapy.
XX
KM Huntingtin's disease; noctropic; anticonvulsant; cytotoxic; mouse.
XX
XX
XX Mus sp.
XX
XX W09960986-AZ.
XX
PD 02-DEC-1999.
XX
XX 27-MAY-1999; 99MO-051143.
XX
XX 27-MAY-1999; 98US-0085199.
XX
PA (OVER-) UNIV BRITISH COLUMBIA.
XX
PA (MER-) MERCK FROSST CANADA INC.
XX
XX Kijichan M. Hayden MR. Beckman A. Chopra V. Nicholson DM.
XX
XX Valdicourt JP. Naegele DM.
XX
XX WPI: 2000-097055/08.
XX
XX N-PSDB: AA258749.
XX
XX Novel proteins useful for treating Huntington's disease by gene therapy

SQ SEQUENCE 180 AA: 17992 MW: 812035203881569 CRC64:
 Query Match 100.0%: Score 559; DB 1; Length 180;
 Best Local Similarity 100.0%: Pred No. 54e-61;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MOAECRGCTGCTGACGPGGPGIPGPGGAGNAGPDEAGTGTGGRGPRAGNAGASGCGCA 60
 Db 1 MOAECRGCTGCTGACGPGGPGIPGPGGAGNAGPDEAGTGTGGRGPRAGNAGASGCGCA 60
 Oy 61 PRPGGAGASGAGCCGACGACGPGESRLLEFLYLPMTPEVLAELASLADAPPLVPG 120
 Db 61 PRPGGAGASGAGCCGACGACGPGESRLLEFLYLPMTPEVLAELASLADAPPLVPG 120
 Oy 121 VLKRFVSGNLTITRLTADNRGLOLSISGLOLSILMWTGCPFLVFLADPPSGQR 180
 Db 121 VLKRFVSGNLTITRLTADNRGLOLSISGLOLSILMWTGCPFLVFLADPPSGQR 180
 RESULT 2
 LAD1_HUMAN STANDARD: PRT: 210 AA.
 LAD1_HUMAN
 1 LAD1_HUMAN 1-210 (rel. 617; Created)
 DT 30-MAY-2000 (rel. 39; Last sequence update)
 DT 16-OCT-2001 (rel. 40; Last annotation update)
 DE LAGE-1 protein.
 CN CMOG OR LAGE1.
 OS Homo sapiens (human)
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP TISSUE:Brain; PubMed:9634360;
 RA Lathin B, Lucas S, Michaux L, de Smet C, Goddard D, Serrano A,
 de Plasen E, Boon T.
 RL LAGE-1, a new gene with tumor specificity.*
 RT Int. J. Cancer 76:903-908(1998).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOPFORMS: LAGE-1A AND LAGE-1B (SHOWN
 HERE); ARE PRODUCED BY DIFFERENT SPLICING
 CC -1- SOME TISSUE SAMPLES OBSERVED IN 25-50% OF TUMOR SAMPLES OF
 MELANOMAS, NON-SMALL-CELL LUNG CARCINOMAS, BLADDER, PROSTATE AND
 CC HEAD AND NECK CANCERS.
 CC -1- DOMAIN: A TRANSMEMBRANE DOMAIN IS PRESENT IN ISOPFORM LAGE-1A.
 CC -1- SIMILARITY: STRONG, TO NY-ESO-1/CXCR.
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 CC DR EMBL_AJ223093: CA11117.1;
 CC DR EMBL_AJ223093: CA11116.1;
 CC DR EMBL_AJ223040: CA11043.1;
 CC DR EMBL_AJ223041: CA11044.1;
 CC Polyomorphism: Alternative splicing; Transmembrane; Antigen.
 CC FT DOMAIN 183 188
 CC FT VARSPPLIC 135 210
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 CC FT
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 CC FT VARIANT 89 89
 CC FT/ID-VAR_007856.

FT VARIANT 138 138 W -> R.
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 SQ SEQUENCE 210 AA: 21119 MW: 8880800A55588E CRC64:
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 Matches 109; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
 Oy 1 MOAECRGCTGCTGACGPGGPGIPGPGGAGNAGPDEAGTGTGGRGPRAGNAGASGCGCA 60
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 Oy 61 PRPGGAGASGAGCCGACGACGPGESRLLEFLYLPMTPEVLAELASLADAPPLVPG 120
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 Oy 121 VLKRFVSGNLTITRLTADNRGLOLSISGLOLSILMWTGCPFLVFLADPPSGQR 180
 Db 121 VLKRFVSGNLTITRLTADNRGLOLSISGLOLSILMWTGCPFLVFLADPPSGQR 180
 RESULT 3
 LAD1_HUMAN STANDARD: PRT: 627 AA.
 LAD1_HUMAN
 1 LAD1_HUMAN 1-627 (rel. 32; Created)
 DT 01-NOV-1995 (rel. 32; Last sequence update)
 DT 16-OCT-2001 (rel. 40; Last annotation update)
 DE Relative polypeptide hydroxylase (EC 1.14.13.-) (WHL ORF VIII).
 CN Relative polypeptide hydroxylase (EC 1.14.13.-) (WHL ORF VIII).
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP TISSUE:Brain; PubMed:9634360;
 RA Lathin B, Lucas S, Michaux L, de Smet C, Goddard D, Serrano A,
 de Plasen E, Boon T.
 RL LAGE-1, a new gene with tumor specificity.*
 RT Int. J. Cancer 76:903-908(1998).
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 CC HEAD AND NECK CANCERS.
 CC -1- DOMAIN: A TRANSMEMBRANE DOMAIN IS PRESENT IN ISOPFORM LAGE-1A.
 CC -1- SIMILARITY: STRONG, TO NY-ESO-1/CXCR.
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 CC DR EMBL_AJ223093: CA11116.1;
 CC DR EMBL_AJ223040: CA11043.1;
 CC DR EMBL_AJ223041: CA11044.1;
 CC Polyomorphism: Alternative splicing; Transmembrane; Antigen.
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